

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/975,123

DATE: 11/01/2001

TIME: 08 41:48

Input Set : A:\ES.txt

Output Set: N:\CRF3\11012001\I975123.raw

3 <110> APPLICANT: Susan M. Freier
 6 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF INSULIN-LIKE GROWTH FACTOR BINDING
 PROTEIN 5
 7 EXPRESSION
 9 <130> FILE REFERENCE: RTS-0253
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/975,123
 C--> 11 <141> CURRENT FILING DATE: 2001-10-09
 11 <160> NUMBER OF SEQ ID NOS: 43
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 20
 16 <212> TYPE: DNA
 17 <213> ORGANISM: Artificial Sequence
 19 <220> FEATURE:
 21 <223> OTHER INFORMATION: Antisense Oligonucleotide
 23 <400> SEQUENCE: 1
 24 tccgtcctcg ctccctcaggg 20
 27 <210> SEQ ID NO: 2
 28 <211> LENGTH: 20
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Artificial Sequence
 32 <220> FEATURE:
 34 <223> OTHER INFORMATION: Antisense Oligonucleotide
 36 <400> SEQUENCE: 2
 37 atgcattctg cccccaagga 20
 40 <210> SEQ ID NO: 3
 41 <211> LENGTH: 1612
 42 <212> TYPE: DNA
 43 <213> ORGANISM: Homo sapiens
 45 <220> FEATURE:
 47 <220> FEATURE:
 48 <221> NAME/KEY: CDS
 49 <222> LOCATION: (44)...(862)
 51 <400> SEQUENCE: 3
 52 ctctctgccc ccaccccgaq gtaaaqqqqg cgaactaaqag aag atg qtg ttg etc 55
 53 Met Val Leu Leu
 54 1
 56 acc ggc qtc etc ctg ctg ctg gcc gcc tat gcg ggg ccg gcc cag agc 103
 57 Thr Ala Val Leu Leu Leu Leu Ala Ala Tyr Ala Gly Pro Ala Gln Ser
 58 5 10 15 20
 60 ctg ggc tcc ttc qtg cac tgc gag ccc tgc gac gag aaa gcc etc tcc 151
 61 Leu Gly Ser Phe Val His Cys Glu Pro Cys Asp Glu Lys Ala Leu Ser
 62 25 30 35
 64 atg tgc ccc ccc agc ccc ctg ggc tgc gag ctg gtc aag gag ccg gcc 199
 65 Met Cys Pro Pro Ser Pro Leu Gly Cys Glu Leu Val Lys Glu Pro Gly

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72 gtc tac acc gag cgc tgc gcc cag ggg ctg cgc tgc ctc ccc cgg cag      295
73 Val Tyr Thr Glu Arg Cys Ala Gln Gly Leu Arg Cys Leu Pro Arg Gln
74      70      75      80
76 gac gag gag aag ccg ctg cac gcc ctg ctg cac ggc cgc ggg gtt tgc      343
77 Asp Glu Glu Lys Pro Leu His Ala Leu Leu His Gly Arg Gly Val Cys
78 85      90      95      100
80 ctc aac qaa aag agc tac cgc gag caa gtc aag atc gag aga gac tcc      391
81 Leu Asn Glu Lys Ser Tyr Arg Glu Gln Val Lys Ile Glu Arg Asp Ser
82      105      110      115
84 cgt gag cac gag gag ccc acc acc tct gag atg gcc gag gag acc tac      439
85 Arg Glu His Glu Glu Pro Thr Thr Ser Glu Met Ala Glu Glu Thr Tyr
86      120      125      130
88 tcc ccc aag atc ttc cgg ccc aaa cac acc cgc atc tcc gag ctg aag      487
89 Ser Pro Lys Ile Phe Arg Pro Lys His Thr Arg Ile Ser Glu Leu Lys
90      135      140      145
92 gct gaa gca gtg aag aag gac cgc aga aag aag ctg acc cag tcc aag      535
93 Ala Glu Ala Val Lys Lys Asp Arg Arg Lys Lys Leu Thr Gln Ser Lys
94      150      155      160
96 ttt gtc ggg gga gcc gag aac act gcc cac ccc cgg atc atc tct gca      583
97 Phe Val Gly Gly Ala Glu Asn Thr Ala His Pro Arg Ile Ile Ser Ala
98 165      170      175      180
100 cct gag atg aga cag gag tct gag cag gcc ccc tgc cgc aga cac atg      631
101 Pro Glu Met Arg Gln Glu Ser Glu Gln Gly Pro Cys Arg Arg His Met
102      185      190      195
104 gag gct tcc ctg cag gag ctc aaa gcc agc cca cgc atg gtg ccc cgt      679
105 Glu Ala Ser Leu Gln Glu Leu Lys Ala Ser Pro Arg Met Val Pro Arg
106      200      205      210
108 gct gtg tac ctg ccc aat tgt gac cgc aaa gga ttc tac aag aga aag      727
109 Ala Val Tyr Leu Pro Asn Cys Asp Arg Lys Gly Phe Tyr Lys Arg Lys
110      215      220      225
112 cag tgc aaa cct tcc cgt ggc cgc aag cgt ggc atc tgc tgg tgc gtg      775
113 Gln Cys Lys Pro Ser Arg Gly Arg Lys Arg Gly Ile Cys Trp Cys Val
114      230      235      240
116 gac aag tac ggg atg aag ctg cca gcc atg gag tac gtt gac ggg gac      823
117 Asp Lys Tyr Gly Met Lys Leu Pro Gly Met Glu Tyr Val Asp Gly Asp
118 245      250      255      260
120 ttt cag tgc cac acc ttc gac agc agc aac gtt gag tga tgcgtccccc      872
121 Phe Gln Cys His Thr Phe Asp Ser Ser Asn Val Glu
122      265      270
124 cccaaaccttt ccccaacccc ctcgaacccc cagccccgac tccagccagc gctccctcc      932
125 accccaggag gccactcatt tcatctcatt taagggaataa atatatatct atctatttga      992
126 ggaacctgag gacctcggaa tctctagaaa ggcctcaact tcgaaaatgg caacaacaga      1052
130 gatgcataaaa gctaaaaaga caaccccccc cttaaataag tttctttttt gaggaagtt      1112
132 gcatqaacag agaaaggaag agaggaagaa cgagaggaag agaaggggaag gaagtgtttg      1172
134 tctagaagag agagaaagac gaatagagtt aggaaaaagga agacaagcag gtqggcagga      1232
136 aggacatgca ccgagaccag qcaggggccc aactttcacg tccagccctg gctqggggtc      1292
138 gggagaggtg ggcgtatgaa gatgcagccc aggatgtgac aatcaatgac actattqggg      1352
140 tttcccagga tggatttqtc agggggagaa agaaaaagac aaaaacactcc aggaactctc      1412
141      142      143      144      145      146      147      148      149      150
142 tttcccagga tggatttqtc agggggagaa agaaaaagac aaaaacactcc aggaactctc      1472

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144 ctettacctg ggcagagtgt tgtctctccc caaatttata aaaactaaaa tgcattccat 1532
146 tctcttgaaa gcaaaacaaa ttcataattg agtqatatta aatagagagq ttttcgqaag 1592
148 cagatctgtg aatatgaaat 1612
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152 <211> LENGTH: 19
153 <212> TYPE: DNA
154 <213> ORGANISM: Artificial Sequence
156 <220> FEATURE:
158 <223> OTHER INFORMATION: PCR Primer
160 <400> SEQUENCE: 4
161 ccaaacacac ccgatctc 19
164 <210> SEQ ID NO: 5
165 <211> LENGTH: 22
166 <212> TYPE: DNA
167 <213> ORGANISM: Artificial Sequence
169 <220> FEATURE:
171 <223> OTHER INFORMATION: PCR Primer
173 <400> SEQUENCE: 5
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177 <210> SEQ ID NO: 6
178 <211> LENGTH: 26
179 <212> TYPE: DNA
180 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
184 <223> OTHER INFORMATION: PCR Probe
186 <400> SEQUENCE: 6
187 aggetgaagc agtgaagaag gaccgc 26
190 <210> SEQ ID NO: 7
191 <211> LENGTH: 19
192 <212> TYPE: DNA
193 <213> ORGANISM: Artificial Sequence
195 <220> FEATURE:
197 <223> OTHER INFORMATION: PCR Primer
199 <400> SEQUENCE: 7
200 gaaggtgaag gtcgagtc 19
203 <210> SEQ ID NO: 8
204 <211> LENGTH: 20
205 <212> TYPE: DNA
206 <213> ORGANISM: Artificial Sequence
208 <220> FEATURE:
210 <223> OTHER INFORMATION: PCR Primer
212 <400> SEQUENCE: 8
213 gaagatggtg atggatttc 20
216 <210> SEQ ID NO: 9
217 <211> LENGTH: 20
218 <212> TYPE: DNA
219 <213> ORGANISM: Artificial Sequence
221 <220> FEATURE:
222 <223> OTHER INFORMATION: PCR Probe

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225 <400> SEQUENCE: 9
226 caaagcttccc gttctcagcc 20
229 <210> SEQ ID NO: 10
230 <211> LENGTH: 1722
231 <212> TYPE: DNA
232 <213> ORGANISM: Homo sapiens
234 <220> FEATURE:
236 <220> FEATURE:
237 <221> NAME/KEY: CDS
238 <222> LOCATION: (752)...(1570)
240 <400> SEQUENCE: 10
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243 ttttcattac cctcctcccg ttttcacctt tctccggact tcgcgtagaa cctgcgaatt 120
245 tcgaagagga ggtggcaaaag tgggagaaaa gaggtgttag ggtttggggg ttttttggtt 180
247 ttgtttttgt tttttaattt cttgatttca acattttctc ccacctctc ggctgcagcc 240
249 aaagctctct accgtgtctg cggggcccgq caccgctgqg agctgagggg tagaaagcgg 300
251 qgtgtatttt agattttaag caaaaatttt aaagataaat ccatttttct ctcaccaccc 360
253 caacgccatc tccactgcac cccatctcat tatttcgggt gttgcttggg ggtgaacaat 420
255 tttgtggctt tttttccctt ataattctga cccgctcagg cttgaggggt tctccggcct 480
257 ccgctcactg cgtgcacctg gcctgcacct gcttccccc aacctgttga aggttttaat 540
259 tcttgcaact gggacctgct cgcaggcacc ccagccctcc acctctctct acatttttgc 600
261 aagtgtctgg gggaggggac ctgctctacc tgcagaaat tttaaaacaa aaacaaaaac 660
263 aaaaaaatct ccggggggcc ttttgcccc tttatccctg cactctcctt cctctgcccc 720
265 accccgaggt aaagggggcg actaagagaa g atg gtg ttg ctc acc gcg gtc 772
266 Met Val Leu Leu Thr Ala Val
267 1 5
269 ctc ctg ctg ctg gcc gcc tat gcg ggg ccg gcc cag agc ctg ggc tcc 820
270 Leu Leu Leu Leu Ala Ala Tyr Ala Gly Pro Ala Gln Ser Leu Gly Ser
271 10 15 20
273 ttc gtg cac tgc gag ccc tgc gac gag aaa gcc ctc tcc atg tgc ccc 868
274 Phe Val His Cys Glu Pro Cys Asp Glu Lys Ala Leu Ser Met Cys Pro
275 25 30 35
277 ccc agc ccc ctg ggc tgc gag ctg gtc aag gag ccg ggc tgc ggc tgc 916
278 Pro Ser Pro Leu Gly Cys Glu Leu Val Lys Glu Pro Gly Cys Gly Cys
279 40 45 50 55
281 tgc atg acc tgc gcc ctg gcc gag ggg cag tgc tgc ggc gtc tac acc 964
282 Cys Met Thr Cys Ala Leu Ala Glu Gly Gln Ser Cys Gly Val Tyr Thr
283 60 65 70
285 gag cgc tgc gcc cag ggg ctg cgc tgc ctc ccc cag cag gac gag gag 1012
286 Glu Arg Cys Ala Gln Gly Leu Arg Cys Leu Pro Arg Gln Asp Glu Glu
287 75 80 85
289 aag ccg ctg cac gcc ctg ctg cac ggc cgc qgg qtt tgc ctc aac gaa 1060
290 Lys Pro Leu His Ala Leu Leu His Gly Arg Gly Val Cys Leu Asn Glu
291 90 95 100
293 aag agc tac cgc gag caa gtc aag atc gag aga gac tcc cgt gag cac 1108
294 Lys Ser Tyr Arg Glu Gln Val Lys Ile Glu Arg Asp Ser Arg Glu His
295 105 110 115
297 gag gag ccc acc acc tct gag atg gcc gag gag acc tac tcc ccc aag 1156
298 Met Met Met Met Met Ser Gln Met Ala Gln Glu Thr Thr Ser Pro Lys

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299 120      125      130      135
301 atc ttc cgg ccc aaa cac acc cgc atc tcc gag ctg aag gct gaa gca 1204
302 Ile Phe Arg Pro Lys His Thr Arg Ile Ser Glu Leu Lys Ala Glu Ala
303      140      145      150
305 gta aag aag gac cgc aga aag aag ctg acc cag tcc aag ttt gtc ggg 1252
306 Val Lys Lys Asp Arg Arg Lys Lys Leu Thr Gln Ser Lys Phe Val Gly
307      155      160      165
309 gga gcc gag aac act gcc cac ccc cgg atc atc tct gca cct gag atg 1300
310 Gly Ala Glu Asn Thr Ala His Pro Arg Ile Ile Ser Ala Pro Glu Met
311      170      175      180
313 aga cag gag tct gag cag gcc ccc tgc cgc aga cac atg gag gct tcc 1348
314 Arg Gln Glu Ser Glu Gln Gly Pro Cys Arg Arg His Met Glu Ala Ser
315      185      190      195
317 ctg cag gag ctc aaa gcc agc cca cgc atg gtg ccc cgt gct gtg tac 1396
318 Leu Gln Glu Leu Lys Ala Ser Pro Arg Met Val Pro Arg Ala Val Tyr
319 200      205      210      215
321 ctg ccc aat tgt gac cgc aaa gga ttc tac aag aga aag cag tgc aaa 1444
322 Leu Pro Asn Cys Asp Arg Lys Gly Phe Tyr Lys Arg Lys Gln Cys Lys
323      220      225      230
325 cct tcc cgt gcc cgc aag cgt gcc atc tgc tgg tgc gtg gac aag tac 1492
326 Pro Ser Arg Gly Arg Lys Arg Gly Ile Cys Trp Cys Val Asp Lys Tyr
327      235      240      245
329 ggg atg aag ctg cca gcc atg gag tac gtt gac ggg gac ttt cag tgc 1540
330 Gly Met Lys Leu Pro Gly Met Glu Tyr Val Asp Gly Asp Phe Gln Cys
331      250      255      260
333 cac acc ttc gac agc agc aac gtt gag tga tgcgtccccc cccaaccttt 1590
334 His Thr Phe Asp Ser Ser Asn Val Glu
335      265      270
337 cctcaccccc ctcccacccc cagcccccagc tccagccagc gcctccctcc accccaggac 1650
339 gccactcatt tcattctcatt taagggaataa atatatatct atctatttga ggaaaaaaaa 1710
341 aaaaaaaaaa aa 1722
344 >210> SEQ ID NO: 11
345 >211> LENGTH: 21000
346 >212> TYPE: DNA
347 >213> ORGANISM: Homo sapiens
349 >220> FEATURE:
352 >400> SEQUENCE: 11
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355 gtcttccact ggcctctcca cctctctccc attctcggta gcccagcct gtccccccttg 120
357 ggccttctctt acattccggg ggaaggaagg ccttgttcaq aggggaagaa ggcctgtttc 180
359 agggagcgaa gggagacccc ctgtgtctta gaagcctctt ccccaccccc acccgtgtg 240
361 agtttgtact gcaaagctcc ttggcctctt tgcctgaatt gqgtgttggg aaqctcaaat 300
363 tgcagctaca aactggtctg cagccagggg ccgctatatt aaaagcgcct gctctcccg 360
365 agccccgtag tctctttgga aactttctga ggggaaaaga gctaggaag agctgcaag 420
367 cagtgtgggc ttttccctt tttgtctctt ttccattacc cctctccgt tttccacctt 480
369 ctccggactt cgcgtagaac ctgcgaattt cgaagagag gtggcaaaat gggagaaaag 540
371 aggtatttag gtttggggtt tttttgtttt tgtttttgtt ttttaatttc ttgatttcaa 600
373 cattttctcc caccctctc gctgcagcca acgcctctta cctgttctgc ggcgcgcgc 660
375 ctttttctcc ctttttctcc ctttttctcc ctttttctcc ctttttctcc ctttttctcc 720

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VERIFICATION SUMMARY

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Input Set A:\ES.txt

Output Set N:\CRF3\11012001\I975123.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date